

# FIG. 1A

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-320          -300          -280
CACTCGTCTGCCCTGGACTCCCGTCTCCTCCTGTCTCCGGCTTCCAGAGCTCCCTCC
+-----+-----+-----+-----+-----+-----+-----+
GTGAGCAGACGGGGACCTGAGGGCAGAGGAGACAGGAGGCCCAAGGGTCTCGAGGGAGG
-260          -240          -220
TTATGGCAGCAGCTTCCCGGTCTCCGGCGCAGTTCTCAGCGGACGACCCCTCTCGGTCCG
+-----+-----+-----+-----+-----+-----+-----+
AATACCGTCTCGAAGGGCGCAGAGGCCGCGTCAAGAGTCGCCCTGCTGGGAGAGCGAGGC
-200          -180          -160
GGGCTGAGCCCACTCCCTGGATGTTGCTGAACCTCTCGAGATCATGCCGGGGTTTGGCTG
+-----+-----+-----+-----+-----+-----+-----+
CCCGACTCGGGTCAGGGACCTACAACGACTTTGAGAGCTCTAGTACGGCCCCCAAACCGAC
-140          -120          -100
CTGCTTCCCCCGGGTGCCCACTGCCACCGCCGCCGCCCTCTGCTGCCGCCGTCCGGGGA
+-----+-----+-----+-----+-----+-----+-----+
GACGAAGGGCGGCCACGGTGACGGTGCGCGCGCGGAGACGACGGCGGCAGGGGCCCT
-80          -60          -40
TGCTCAGTAGCCCGCTGCCCGGCCCGCGATCCTGTCTCCTCGAAGCCGTTTGCTGC
+-----+-----+-----+-----+-----+-----+-----+
ACGAGTCATCGGGCGACGGCGCGGGCGGCTAGGACACAAAGGAGCCCTTCGGCAACGACG
-20          0          20
MATCH WITH FIG. 1B

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FIG. 1B

MATCH WITH FIG. 1A

TGCAGAGTTGCACGAAC TAGTCATGTCGTGGAGTCCCCGGCAGTGCACAGCTG  
 +-----+-----+-----+-----+-----+-----+  
 ACGTCTCAACGTGCTGATCAGTACCAACGACACCCCTCAGGGCGCCGTCACGTCGTCGAC  
 M V L W E S P R Q C S S W  
 40 : 60 80

GACACTTTGCGAGGGCTTTTGGCTGGCTGCTGCTGCTGCCGCTCATGCTACTCATCGTAGC  
 CTGTGAAACGCTCCCGAAACGACCGACGACGACGACGGCGACGTACGATGAGTAGCATCG  
 T L C E G F C W L L L L L L P V M L L L I V A  
 100 120 140

CGGCCGGTGAACTCGCTGCTTTCCCTACCTCCTTAAGTACTGCCAAACGCCACCGG  
 +-----+-----+-----+-----+-----+-----+-----+-----+  
 GCGGGCCACTTCGAGCGACGAAAGGATGGAGGAAATTCACTGACGGTTTGCGGGTGGCC  
 R P V K L A A F P T S L S D C Q T P T G  
 160 180 200

CTGGAATTGCTCTGGTTATGATGACAGAGAAAATGATCTCTTCTCTGTGACACCAACAC  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 GACCTTAAACGAGACCAATACTACTGTCTCTTTTACTAGAGAAGGAGACACACTGTGGTTGTG  
 W N C S G Y D D R E N D L F L C D T N T  
 220 240 260

CTGTAAATTTCATCGGGAATGTTTAAGAAATTGGAGACACTGTGACTTCCGCTCTGTCAGTTT  
MATCH WITH FIG. 1C

# FIG. 1C

MATCH WITH FIG. 1B

```

+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GACATTTAAACTACCCCTTACAAATTCTTAACCTCTGTGACACTGAACGCAGACAGTCAA
C K F D G E C L R I G D T V T C V C Q F
280 300 320

CAAGTGCAACAATGACTATGTGCCCTGTGTGGCTCCAATGGGGAGAGCTACCAGAAATGA
+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GTTACCGTTGTTACTGATACACGGACACACACCGAGGTTACCCCTCTCGATGGTCTTACT
K C N N D Y V P V C G S N G E S Y Q N E
340 360 380

GTGTTACCTGCGACAGGCTGCATGCAACACAGCAGAGTGAGATACTTGTGGTGCAGAAGG
+-----+-----+-----+-----+-----+-----+-----+-----+-----+
CACAATGGACGCTGTCCGACGTACGTTTGTGCTCTCACTCTATGAACACCACAGTCTTCC
C Y L R Q A A C K Q Q S E I L V V S E G
400 420 440

ATCATGTGCCACAGATGCAGGATCAGGATCTGGAGATGGAGTCCATGAAGGCTCTGGAGA
+-----+-----+-----+-----+-----+-----+-----+-----+-----+
TAGTACACGGTGTCTACGTCCTAGTCCTAGACCTCTACCTCAGGTACTTCCGAGACCTCT
S C A T D A G S G S G D G V H E G S G E
460 480 500

AACTAGTCAAAAGGAGACATCCACCTGTGATATTGGCCAGTTTGGTGCAGAAATGTGACGA
+-----+-----+-----+-----+-----+-----+-----+-----+-----+
TTGATCAGTTTTCCTCTGTAGGTGGACACTATAAACGGTCAAAACCACGTCTTACACTGCT

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MATCH WITH FIG. 1D

MATCH WITH FIG. 1C

T S Q K E T S T C D I C Q F G A E C D E  
520 540 560

AGATGCCGAGGATGCTGCTGCTGCTGTAATATTGACTGTTCTCAAACCAACTCAATCC  
+-----+-----+-----+-----+-----+-----+-----+-----+  
TCTACGGCTCCTACAGACCACACACATATTAACCTGACAAGAGTTGGTTGAAGTTAGG  
D A E D V W C V C N I D C S Q T N F N P  
580 600 620

CCTCTGCGCTTCTGATGGGAATCTTATGATAATGCATGCCAAATCAAAGAAGCATCGTG  
+-----+-----+-----+-----+  
GGAGACGCGAAGACTACCCTTTAGATACTATTACGTACGGTTAGTTCTTCGTAGCAC  
L C A S D G K S Y D N A C Q I K E A S C  
640                  660                  680

TCAGAAACAGGAGAAATTGAAGTCATGTCTTTGGTCGATGTC AAGATAACACAAC TAC  
AGTC TTTTGTCCTCTTTTAAC TTCAGTACAGAAACCCAGCTACAGTTC TATGTTGTTGATG  
Q K Q E K I E V M S L G R C Q D N T T T  
700 720 740

AACTACTAAGTCTGAAGATGGGCATTATGCAAGAACAGATTATGCAGAGAAATGCTAACAA  
 TTGATGATTGATTCAGACTTCTACCCGTAATACGTTCTTGCTCTAATACGTTCTCTTACGATTGTT  
 T T K S E D G H Y A R T D Y A E N A N K  
 760 780 800

MATCH WITH FIG. 1E

# FIG. 1E

MATCH WITH FIG. 1D

ATTAGAAAGTGCCAGAGAACACCACATACCTTGTCGGAACATTACAAATGGCTTCTG  
 TAATCTTCTTTCACGGTCTCTTGTTGGTGTATGGAACAGGCCCTGTAATGTACCGAAGAC  
 L E S A R E H H I P C P E H Y N G F C  
 820 840 860

CATGCATGGGAAGTGTAGCAATTCATCAATATGCAGGAGCCCATCTTGCAGGTGTGATGC  
 GTACGTACCCCTTCACACTCGTAAGATAGTTATACGTCCCTCGGTAGAACGTCCACACTACG  
 M H G K C E H S I N M Q E P S C R C D A  
 880 900 920

TGGTTATACTGGACAACACTGTGTGAAAAAAGGACTACAGTGTCTTATACGTGTGTTCCCGG  
 ACCAATATGACCTGTTGTGACACTTTTTTTCCTGATGTCACAAGATATGCAACAAGGGCC  
 G Y T G Q H C E K K D Y S V L Y V V P G  
 940 960 980

TCCTGTACGATTTCAGTATGTCTTAAATCGCAGCTGTGATTGGAACAATTTCAGATTGCTGT  
 AGGACATGCTAAAGTCATACAGAAATTAGCGTCGACACTAACCTTGTTAAGTCTAACGACA  
 P V R F Q Y V L I A A V I G T I Q I A V  
 1000 1020 1040

CATCTGTGTGGTGCTCCTCTGCATCACAAAGGAAATGCCCCAGAAAGCAACAGAATTTCACAG  
 GTAGACACACCACGAGACGTAGTGTTCCTTTACGGGGTCTTTCGTTGTCTTAAAGTGTG  
 MATCH WITH FIG. 1F

MATCH WITH FIG. 1E

I	C	V	V	V	L	C	I	T	R	K	C	P	R	S	N	R	I	H	R
1060							1080									1100			
ACAGAAGCAAAATACAGGCACTACAGTTCGGACAATACAACAAGAGCGTCCACGAGGTT																			
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+																			
TGCTTCGTTTATGTCCCGTGATGTCAAGCCCTGTTATGTTGTTCTCGCAGGTGCTCCAA																			
Q	K	Q	N	T	G	H	Y	S	S	D	N	T	T	R	A	S	T	R	L
1120							1140									1160			
AATCTAAAGGGAGCATGTTTCACAGTGGCTGGACTACCGAGAGCTTGGACTACACAATAC																			
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+																			
TTAGATTTCCCTCGTACAAAGTGTCAACCGACCTGATGGCTCTCGAACCTGATGTTTATG																			
I	*																		
1180							1200									1220			
AGTATTATAGACAAAGAATAAGACAAGAGATCTACACATGTTGCCCTTGCAATTTGTGGTA																			
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+																			
TCATAATATCTGTTTTCTTATTCGTCTCTAGATGTGTACAAACGGAACGTAAACACCAT																			
1240							1260									1280			
ATCTACACCAATGAAACATGTACTACAGCTATATTTTGATTATGTATGGATATATTTGAA																			
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+																			
TAGATGTGGTTACTTTTGTACATGATGTGCGATATAAACTAATACATACCTATATATAAACTT																			
1300							1320									1340			
ATAGTATACATGTCTTGATGTTTTTTTCTGTAATGTAATAAACTATTTATATCACACAA																			
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+																			
TATCATATGTAAACAGAACTACAAAAAAGACATTACATTTATTGATAAAATATAGTGTGTT																			
1360																			
AAAAA																			
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+																			
TTTTTTTTTTTTTTTT																			

FIG. 1F

# FIG. 2A

	M	V	-	-	-	X	X	X	C	S	S	-	-	-	-	-	-	-	A	X	X	L	L	L	L	X	X	A	L	G	Majority	
1	M	D	-	-	-	R	A	R	C	S	G	-	-	-	-	-	-	-	A	S	S	L	P	L	L	L	A	L	A	L	G	hBCp
11	M	V	-	-	-	-	-	-	-	P	S	-	-	-	-	-	-	-	A	G	Q	L	A	L	F	-	-	-	A	L	G	hTGFap
11	M	V	L	W	E	S	P	R	Q	C	S	S	W	T	L	C	E	G	F	C	W	L	L	L	L	P	V	M	L	L	L	TGFa95.aa
	I	V	-	-	-	-	-	-	-	-	-	-	-	L	X	X	C	Q	X	X	X	G	X	X	X	X	X	-	-	-	-	Majority
23	L	V	-	-	-	-	-	-	-	-	-	-	I	L	H	C	V	V	A	D	G	N	S	T	R	S	-	-	-	-	-	hBCp
15	I	V	-	-	-	-	-	-	-	-	-	-	L	A	A	C	Q	A	L	E	N	S	T	S	P	-	-	-	-	-	-	hTGFap
31	I	V	A	R	P	V	K	L	A	A	F	P	T	S	L	S	D	C	C	O	T	P	T	G	W	N	C	S	G	Y	D	TGFa95.aa
	-	X	E	X	X	X	L	C	X	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Majority
39	-	P	E	T	N	G	L	L	C	G	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hBCp
30	-	-	-	-	-	-	-	-	L	S	A	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hTGFap
61	D	R	E	N	D	L	F	L	C	D	T	N	T	C	K	F	D	G	E	C	L	R	I	G	D	T	V	T	C	V	-	TGFa95.aa
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Majority
49	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hBCp
34	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hTGFap

MATCH WITH FIG. 2B

MATCH WITH FIG. 2B

MATCH WITH FIG. 2A		FIG. 2B	
91	C Q F K C N N D Y V P V C G S N G E S Y Q N E C Y L R Q A A	TG Fa95.aa	
	- - - - - P E X X C A X - - - - -	Majority	
	130 140 150		
49	- - - - - P E N C A A - - - - -	hBCp	
34	- - - - - P P V A A V - - - - -	hTG Fap	
121	C K Q Q S E I L V S E G S C A T D A G S G S G D G V H E G	TG Fa95.aa	
	- - - - -	Majority	
	160 170 180		
56	- - - - -	hBCp	
41	- - - - -	hTG Fap	
151	S G E T S Q K E T S T C D I C Q F G A E C D E D A E D V W C	TG Fa95.aa	
	- - - - -	Majority	
	190 200 210		
56	- - - - -	hBCp	
41	- - - - -	hTG Fap	
181	V C N I D C S Q T N F N P L C A S D G K S Y D N A C Q I K E	TG Fa95.aa	
	- - - - - T T T X X X X X G	Majority	
	220 230 240		
MATCH WITH FIG. 2C			





MATCH WITH FIG. 2C

# FIG. 2D

	X	X	I	X	X	C	V	X	X	X	C	C	X	-	X	R	K	X	C	X	R	X	X	X	X	X	X	E	Majority		
134	L	V	I	G	V	C	T	-	-	-	C	C	H	P	L	R	R	R	R	K	K	-	-	-	-	K	E	E	hBCp		
113	V	L	I	T	C	V	L	I	H	C	C	C	Q	-	V	R	K	H	C	E	W	C	R	A	L	I	C	R	H	E	hTGFap
331	I	A	V	-	I	C	V	V	L	C	-	-	-	I	T	R	K	C	P	R	S	N	R	I	H	R	Q	K	Q	TGfa95.aa	
	X	X	X	L	X	K	D	X	T	X	X	-	-	X	X	X	X	X	X	X	I	X								Majority	
157	E	M	E	T	L	G	K	D	I	T	P	I	N	E	D	I	E	E	T	N	I	A								hBCp	
142	K	P	S	A	L	L	K	G	R	T	A	C	-	-	-	C	H	S	E	T	V	V								hTGFap	
357	N	T	G	H	Y	S	S	D	N	T	T	-	-	-	R	A	S	T	R	L	I									TGfa95.aa	

10 / 10

Decoration 'Decoration #1': Shade with solid residues that match the Consensus exactly.